REMARKS

Applicants have substituted into the present specification a new paper copy Sequence Listing section according to 37 C.F.R. §1.821(c) as new pages 1-8.

Applicants have amended the previously filed Sequence Listing and revised Figures 1, 2A, 5, 7 and 8 to make them conform to the amended Sequence Listing.

SEQ ID NO:1 of the previously filed Sequence Listing corresponded to originally filed Figure 1. Originally filed Figure 1 erroneously duplicated the lower nucleotide sequence presented in Figure 4 (which lower sequence now corresponds to SEQ ID NO:4 in the attached substitute Sequence Listing). SEQ ID NO:1 of the Sequence Listing and Figure 1 have been amended to conform to the nucleotide sequence shown Figs. 2A (lower sequence), 5, 7 and 8. These amendments are supported by the disclosure in the specification of Figs. 1, 2A, 5, 7 and 8, that SEQ ID NO:1 is identical in all these figures.

The amendment to SEQ ID NO:2 was necessitated due to an erroneous addition of incorrect nucleotides at positions 886-953. These incorrect nucleotides have now been deleted from SEQ ID NO:2 and this amendment is supported by the nucleotide sequence shown in Figure 2A (upper sequence).

SEQ ID NO:3 has been deleted from the previously filed Sequence Listing as SEQ ID NO:3 was a partial sequence of SEQ ID NO:1. The subsequent sequences have been renumbered accordingly in the attached substitute Sequence Listing.

The revisions to Figs. 1, 2A and 5 were necessitated due to typographical/clerical errors made when drafting these figures, and were made to make the sequences of Figs. 1, 2A and 5 conform to SEQ ID NO:1.

The revisions to Figures 7 and 8 merely correct an alignment error in the second column of the last row of the sequence.

All of the above revisions to the Sequence Listing and the figures are of clerical/typographical nature and do not constitute new matter. Approval of all of the revisions is therefore respectfully requested.

Furthermore, attached hereto is a 3 1/2" disk containing the "Sequence Listing" in computer readable form in accordance with 37 C.F.R. §1.821(e).

Applicants have amended the specification to insert SEQ ID Nos, as supported in the present specification.

The following statement is provided to meet the requirements of 37 C.F.R. \$1.825(a) and 1.825(b).

I hereby state, in accordance with 37 C.F.R. §1.825(a), that the amendments included in the substitute sheets of the sequence listing are believed to be supported in the application as filed and that the substitute sheets of the sequence listing are not believed to include new matter.

I hereby further state, in accordance with 37 C.F.R. \$1.825(b), that the attached copy of the computer readable form is the same as the attached substitute paper copy of the sequence listing.

Under U.S. rules, each sequence must be classified in <213> as an "Artificial Sequence", a sequence of "Unknown" origin, or a sequence originating in a particular organism, identified by its scientific name.

Neither the rules nor the MPEP clarify the nature of the relationship which must exist between a listed sequence and an organism for that organism to be identified as the origin of the sequence under <213>.

Hence, counsel may choose to identify a listed sequence as associated with a particular organism even though that sequence does not occur in nature by itself in that organism (it may be, e.g., an epitopic fragment of a naturally occurring protein, or a cDNA of a naturally occurring mRNA, or even a substitution mutant of a naturally occurring sequence). Hence, the identification of an organism in <213> should not be construed as an admission that the sequence per se occurs in nature in said organism.

Similarly, designation of a sequence as "artificial" should not be construed as a representation that the sequence has no association with any organism. For example, a primer or probe may be designated as "artificial" even though it is necessarily complementary to some target sequence, which may occur in nature. Or an "artificial" sequence may be a substitution mutant of a natural sequence, or a chimera of two or more natural sequences, or a cDNA (i.e., intron-free sequence) corresponding to an intron-containing gene, or otherwise a fragment of a natural sequence.

The Examiner should be able to judge the relationship of the enumerated sequences to natural sequences by giving full consideration to the specification, the art cited therein, any further art cited in an IDS, and the results of his or her sequence search against a database containing known natural sequences.

Attached hereto is a marked-up version of the changes made to the specification by the current amendment.

The attached page is captioned "Version with markings to show changes made".

Applicants submit that the present application contains patentable subject matter and therefore urge the examiner to pass the case to issuance.

If the examiner has any questions or comments concerning the above described application, the examiner is urged to contact the undersigned at the phone number below.

Respectfully submitted,

BROWDY AND NEIMARK, P.L.L.C.
Attorneys for Applicant(s)

Attorneys for Applicant(s)

ALLEN C. YUN

Registration No. 37,971

ACY:al

624 Ninth Street, N.W.

Washington, D.C. 20001

Telephone No.: (202) 628-5197 Facsimile No.: (202) 737-3528

F:\,C\cohn\moroz3\pto\RESPONSE TO NOTICE TO COMPLY.doc

VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the specification:

The table on page 15 has been amended as follows:

5' GGT GGC GAC GAC TCC TGG AGC CCG 3' 5' TTG ACA CCA GAC CAA CTG GTA ATG 3' 5' GAC CGC GAT GAT GTG GCT TTG AAG AAC 3' 5' GAC AGG ATC TTT AGC GAC AGC CGA 3' 5' GAT AGG ATC TTT AGC GAC AGC CGA 3' 5' CGG GCT CTT GAG TCC TGG TGG 3' 5' CGG GCT GAA TGC AAT GGA GTG TGC 3' 5' CGG GCT GAA TGC AAT GGA GTG TGC 3' 5' GAC CCC CAT TTG TGT GAC 3' 5' GAC CCC CAT TTG TGT GAC 3' 5' Biotin-TTG ACA CCA GAC CAA CTC GTA ATG 3' 5' GAC CGC GAC CGA GAC CAA CTC GTA ATG 3' 5' GTT CTT CAA AGC CAC ATC ATC GGA GTG 3' 5' GTT CTT CAA AGC CAC ATC ATC GGG GTC 3' 5' GTT CTT CAT ATC ACT GTC TCC CAG GGT G 3' 5' CAG ACG TTC TTC GCC GAG AGT CGT 3' 5' CAG ACG TTC TTC GCC GAG AGT CGT 3' 5' CAG ACG TTC TTC GCC GAG AGT CGT 3' 5' CAT TCC GGG GA AC CCG GCG T 3' 5' CAT TCC GGG GAAC CCG GGT GGG AGC CGT 3' 5' CCT TTC ACT ACT ACT GCG GGT GGG AGC CGT ACCCC GGG AAC CCG GCG CT 3' 5' CGG GAC GGA ACCCG GCG CT 3' 5' CGC TCT ACA CTT ATC ATC TCC AGG GTG GGG GGG AGCCC TCCC CGG GCG CT GCG GGG GGG AGCCCG GGG AGCCCG GGG GGG G		
5' GAC CGC GAT GAT GTG GCT TTG AAG AAC 3' 5' GAT AGG ATC TTT AGC GAC AGC CGA 3' 5' GAT AGG ATC TTT AGC GAC AGC CGA 3' 5' ATG GCG GCC TCT GAG TCC TGG TGG 3' 5' CGG GCT GAA TGC AAT GGA GTG TGC 3' 5' CGA CGC CAT TTG TGT GAC 3' 5' CGA CGA CTC CTG GAG CCC G 3' 5' Biotin-TTG ACA CCA GAC CAA CTC GTA ATG 3' 5' Biotin-TTG ACA CCA GAC CAA CTC GTA ATG 3' 5' GTT CTT CAA AGC CAC ATC ATC GCG GTC 3' 5' GTT CTT CAA AGC CAC ATC ATC GCG GTC 3' 5' CAG ACG TTC TTC GCC GAG AGT CGT 3' 5' CAG ACG TTC TTC GCC GAG AGT CGT 3' 5' CAG ACG TTC TTC GCC GAG AGT CGT 3' 5' CAT TTC GGG GAT TCG GGG GA 3' 5' CAT TTC GGG GAT TCG GGG GT 3' 5' CAT TTC GGG GAT TCG GGG GTC 3' 5' CAT TTC GGG GAT TCG GGG GTC 3' 5' CAT TTC GGG GAT TCG GGG GTC 3' 5' CAT TTC GGG GAT TCG GGG GA 3' 5' CAT TTC GGG GAT TCG GGG GTC 3' 5' CAT TTC GGG GAT TCG GGG GTC 3' 5' CAT TTC GGG GAT TCG GGG GA 3' 5' GTG ACG TTC TTC GCC GAG AGT CGT CGG 3' 5' GTG AAA TCG CTG TCG TCG GCT 3' 5' CTA TCC TAG AAA TCG CTG TCG GCT 3' 5' GTC ACT ACT GGA ATT CCC TTC TCC 3' 5' GGA GAA GGG AAT TCC AGT AGT GAC 3' 5' GGG GAAA GGG AAT TCC AGT AGT GAC 3' 5' GGG GAAA TCG CTG TCG CCTA ACC 3' 5' GGG CAC GCG ACA GCG ATT TCC 3' 5' GGC CAC GCG TCG ACT AGT ACC 3' 5' GGC CAC GCG TCG ACT AGT ACC 3' 5' GTA ATG CAC ACT CCA TTG GC 5' GGA AAT CGC TGG ACT AGT ACC 3' 5CQ.ID.NO.22 5' GTA ATG CAC ACT CCA TTG GC 5' GGA ATT CCA GCT GAG CGC GC 5' GGA ATT CCA GCT GAG CGC GCC 5' GGA CCC CCA TGA CGC GGC CGC CGC CCC CCC CCC GCCCCC 5' GCC TCC AGC TGA CCGA CAGC GGT CCA CCC GCCCCCCCCCC	5' GGT GGC GAC GAC TCC TGG AGC CCG 3'	SEQ.ID.NO:6
5' GAT AGG ATC TTT AGC GAC AGC CGA 3' 5' ATG GCG GCC TCT GAG TCC TGG TGG 3' 5' CGG GCT GAA TGC AAT GGA GTG TGC 3' 5' CGG GCT GAA TGC AAT GGA GTG TGC 3' 5' CGA CGA CTC CTG GAG CCC G 3' 5' Biotin-TTG ACA CCA GAC CAA CTC GTA ATG 3' 5' Biotin-TTG ACA CCA GAC CAA CTC GTA ATG 3' 5' GTT CTT CAA AGC CAC ATC ATC GCG GTC 3' 5' GTT CTT CAA AGC CAC ATC ATC GCG GTC 3' 5' CAG ACG TTC TTC GCC GAG AGT CGT 3' 5' CAG ACG TTC TTC GCC GAG AGT CGT 3' 5' CAG ACG TTC TTC GCC GAG AGT CGT 3' 5' CAG ACG TTC TTC GCC GAG AGT CGT 3' 5' CAT TTC GGG GAT TCT TC GCC GAG AGT CGT 3' 5' CAT TTC GGG GAT TCT TC GCC GAG AGT CGT 3' 5' CAT TTC GGG GAT TCT GGC GCG TG 3' 5' CAT TTC GGG GAT TCT GGC GAG AGT CGT 3' 5' CTC TCT ACA CTT ATC ATC TCT 3' 5' CTC TCT ACA CTT ATC ATC TCT 3' 5' CTA TCC TAG AAA TCG CTG TCG GCT 3' 5' GTC ACT ACT GGA ATT CCC TTC TCC 3' 5' GTC ACT ACT GGA ATT CCC TTC TCC 3' 5' GGA GAA GGG AAT TCC AGT AGT GAC 3' 5' GGC GAC GGA CGG ACT ACC 3' 5' GGC CAC GCG TCG ACT ACC 3' 5' GGC CAC GCG TCG ACT AGT ACC 3' 5' GGC CAC GCG TCG ACT AGT ACC 3' 5' GGC CAC GCG TCG ACT AGT ACC 3' 5' GTA ATG CAC ACT CCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG GC GCT CCA CC 3' 5' GTA ATG CAC ACT CCA TTG GC GCT CCA CC 3' 5' GTA ATG CAC ACT CCA TTG GC GCT CCA CC 3' 5' GTA ATG CAC ACT CCA TTG GC GCT CCA CC 3' 5' GTG GGA TCC CCA TGA CGA CGG CGT CCA CC 3' 5' GTG GGA TCC CCA TGA CGA CGG CGT CCA CC 3' 5' GTG GGA TCC CCA TGA CGA CGG CGT CCA CC 3' 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC A	5' TTG ACA CCA GAC CAA CTG GTA ATG 3'	SEQ ID NO:7
5' ATG GCG GCC TCT GAG TCC TGG TGG 3' 5' CGG GCT GAA TGC AAT GGA GTG TGC 3' 5' GAC CCC CAT TTG TGT GAC 3' 5' CGA CGA CTC CTG GAG CCC G 3' 5' Biotin-TTG ACA CCA GAC CAA CTC GTA ATG 3' 5' AGC CGA CAG CGA TTT CTA GGA TAG 3' 5' GTT CTT CAA AGC CAC ATC ATC GCG GTC 3' 5' GCT TTC ATT ATC ACT GTC TCC CAG GGT G 3' 5' CAG ACG TTC TTC GCC GAG AGT CGT 3' 5' CAG ACG TTC TTC GCC GAG AGT CGT 3' 5' CAG ACG TTC TTC GCC GAG AGT CGT 3' 5' CAT TTC GGG GAT TCG GGG GA 3' 5' CAT TTC GGG GAT TCG GGG GA 3' 5' CAT TTC GGG GAT TCG GGG GA 3' 5' CAT TTC GGG GAT CGT GGG GA 3' 5' CAT TCC TAG AAA TCG CTG TCG GCT 3' 5' CCC TCT ACA CTT ATC ATC TTC 3' 5' CTA TCC TAG AAA TCG CTG TCG GCT 3' 5' CTA TCC TAG AAA TCG CTG TCG GCT 3' 5' GGA GAA GGG AAT TCC AGT AGT GAC 3' 5' GGA CAC GCG CTA ACC 3' 5' GGA CAC GCG TCG ACT AGT ACC 3' 5' GGC CAC GCG TCG ACT AGT ACC 3' 5' GGC CAC GCG TCG ACT AGT ACC 3' 5' GGC CAC GCG TCG ACT AGT ACC 3' 5' GGC CAC GCG TCG ACT AGT ACC 3' 5' GGA AAT CGC TGT CGC CTA ACC 3' 5' GGA ATG CAC ACT CCA TTG GC 3' 5' GGA ATG CAC ACT CCA TTG GC 3' 5' GGA ATG CAC ACT CCA TTG GC 3' 5' GGA ATG CAC ACT CCA TTG GC 3' 5' GGA ATG CAC ACT CCA TTG GC 3' 5' GGA ATG CAC ACT CCA TTG GC 3' 5' GGA ATG CAC ACT CCA TTG GC 3' 5' GGA ATG CAC ACT CCA TTG GC 3' 5' GGA ATT CCA GCT GAC ACT CCA TTG GC 3' 5' GGA ATT CCA GCT GAC ACT CCA TTG GC 3' 5' GGA ATT CCA GCT GAC ACT CCA TTG GC 3' 5' GGA ATT CCA GCT GAC ACT CCA TTG GC 3' 5' GGA ATT CCA GCT GAC ACT CCA TTG GC 3' 5' GGA ATT CCA GCT GAC ACC CCA TTG GC GCT CCA CC GCT CCA CCA GCG TCCA CCA GCG GCG TCCA CCG GCG TC	5' GAC CGC GAT GAT GTG GCT TTG AAG AAC 3'	SEQ ID NO:8
5' CGG GCT GAA TGC AAT GGA GTG TGC 3' 5' GAC CCC CAT TTG TGT GAC 3' 5' CGA CGA CTC CTG GAG CCC G 3' 5' Biotin-TTG ACA CCA GAC CAA CTC GTA ATG 3' 5' AGC CGA CAG CGA TTT CTA GGA TAG 3' 5' GTT CTT CAA AGC CAC ATC ATC GCG GTC 3' 5' GTT CTT CAA AGC CAC ATC ATC GCG GTC 3' 5' CAG ACG TTC TTC GCC GAG AGT CGT 3' 5' CAG ACG TTC TTC GCC GAG AGT CGT 3' 5' CAG ACG TTC TTC GCC GAG AGT CGT 3' 5' CAT TTC GGG GAT TCG GGG GA 3' 5' CAT TTC GGG GAT TCG GGG GA 3' 5' CAT TTC GGG GAT TCG GGG GA 3' 5' CAT TTC GGG GAT CGT GGG GA 3' 5' CAT TTC GGG GAAC CCG GCG CT 3' 5' CCC TCT ACA CTT ATC ATC TTC 3' 5' CTA TCC TAG AAA TCG CTG TCG GCT 3' 5' GTC ACT ACT GGA AAT CCC TTC TCC 3' 5' GGA GAA GGG AAT TCC AGT AGT GAC 3' 5' GGA CAC GCG TCG ACT AGT ACC 3' 5' GGC CAC GCG TCG ACT AGT AC 3' 5' GTA ATG CAC ACTCCA TTG GC 3' 5' GTA ATG CAC ACTCCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG GC 3' 5' GGA AAT CCC TGG ACT AGT AC 3' 5' GTA ATG CAC ACT CCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG 3' 5' GAG ATT CCA GCT GAG CGC 3' 5' GGA ATT CCA GCT GAG CGC 3' 5' GAG ATT CCA GCT GAG CGC 3' 5' GAG ATT CCA GCT GAG CGC 3' 5' GAG ATT CCA GCT GAG CGC GT CCA CC 3' 5' GAG ATT CCA GCT GAG CGC GAT TTC 3' 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA AATC AG 3'	5' GAT AGG ATC TTT AGC GAC AGC CGA 3'	SEQ ID NO:9
5' GAC CCC CAT TTG TGT GAC 3' SEQ.ID NO.12 5' CGA CGA CTC CTG GAG CCC G 3' SEQ.ID NO.13 5' Biotin-TTG ACA CCA GAC CAA CTC GTA ATG 3' SEQ.ID NO.14 5' AGC CGA CAG CGA TTT CTA GGA TAG 3' SEQ.ID NO.15 5' GTT CTT CAA AGC CAC ATC ATC GCG GTC 3' SEQ.ID NO.16 5' GCT TTC ATT ATC ACT GTC TCC CAG GGT G 3' SEQ.ID NO.17 5' CAG ACG TTC TTC GCC GAG AGT CGT 3' SEQ.ID NO.18 5' CAG ACG TTC TTC GCC GAG AGT CGT 3' SEQ.ID NO.19 5' CAT TTC GGG GAT TCG GGG GA 3' SEQ.ID NO.20 5' GGG GGA CGG AAC CCG GCG CT 3' SEQ.ID NO.21 5' CCC TCT ACA CTT ATC ATC TTC 3' SEQ.ID NO.22 5' CTA TCC TAG AAA TCG CTG TCG GCT 3' SEQ.ID NO.23 5' GTC ACT ACT GGA ATT CCC TTC TCC 3' SEQ.ID NO.24 5' GGA GAA GGG AAT TCC AGT AGT GAC 3' SEQ.ID NO.25 5' GGA GAA GGG ACT GCC CTA ACC 3' SEQ.ID NO.22 5' GGT TAG GCG ACA GCG ATT TCC 3' SEQ.ID NO.22 5' GGT TAG GCG ACA GCG ATT TCC 3' SEQ.ID NO.22 5' GTA ATG CAC ACT CCA TTG 3' SEQ.ID NO.22 5' GTA ATG CAC ACT CCA TTG 3' SEQ.ID NO.30 5' GCG CTC AGC TGG AAT TCC 3' SEQ.ID NO.31 5' GGA ATT CCA GCT GAG CGC 3' SEQ.ID NO.32	5' ATG GCG GCC TCT GAG TCC TGG TGG 3'	SEQ ID NO:10
5' CGA CGA CTC CTG GAG CCC G 3' 5' Biotin-TTG ACA CCA GAC CAA CTC GTA ATG 3' 5' AGC CGA CAG CGA TTT CTA GGA TAG 3' 5' AGC CGA CAG CGA TTT CTA GGA TAG 3' 5' GTT CTT CAA AGC CAC ATC ATC GCG GTC 3' 5' GCT TTC ATT ATC ACT GTC TCC CAG GGT G 3' 5' CAG ACG TTC TTC GCC GAG AGT CGT 3' 5' CAG ACG TTC TTC GCC GAG AGT CGT 3' 5' CAG ACG TTC TTC GCC GAG AGT CGT 3' 5' CAG ACG TTC TTC GCC GAG AGT CGT 3' 5' CAT TTC GGG GAT TCG GGG GA 3' 5' CAT TTC GGG GAT TCG GGG GA 3' 5' CAT TTC GGG GAT TCG GGG GA 3' 5' CCC TCT ACA CTT ATC ATC TTC 3' 5' CCC TCT ACA CTT ATC ATC TTC 3' 5' GTC ACT ACT GGA AAT CCC TTC TCC 3' 5' GGA GAA GGG AAT CCC TTC TCC 3' 5' GGA GAA GGG AAT TCC AGT AGT GAC 3' 5' GGA GAA GGG ACT CGC CTA ACC 3' 5' GGT TAG GCG ACA GCG ATT TCC 3' 5' GGC CAC GCG TCG ACT AGT AC 3' 5' GTA ATG CAC ACT CCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG 3' 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3'	5' CGG GCT GAA TGC AAT GGA GTG TGC 3'	SEQ ID NO:11
5' Biotin-TTG ACA CCA GAC CAA CTC GTA ATG 3' 5' AGC CGA CAG CGA TTT CTA GGA TAG 3' 5' GTT CTT CAA AGC CAC ATC ATC GCG GTC 3' 5' GCT TTC ATT ATC ACT GTC TCC CAG GGT G 3' 5' CAG ACG TTC TTC GCC GAG AGT CGT 3' 5' CAG ACG TTC TTC GCC GAG AGT CGT 3' 5' CAG ACG TTC TTC GCC GAG AGT CGT 3' 5' CAT TTC GGG GAT TCG GGG GA 3' 5' CAT TTC GGG GAT TCG GGG GA 3' 5' CAT TTC GGG GAT TCG GGG GA 3' 5' CAT TTC GGG GAT TCG GGG GA 3' 5' CCC TCT ACA CTT ATC ATC TTC 3' 5' CCC TCT ACA CTT ATC ATC TTC 3' 5' GTC ACT ACT GGA AAT CCC TTC TCC 3' 5' GGA GAA GGG AAT TCC AGT AGT GAC 3' 5' GGA AAT CGC TGT CGC CTA ACC 3' 5' GGT TAG GCG ACA GCG ATT TCC 3' 5' GGC CAC GCG TCG ACT AGT AC 3' 5' GGC CAC GCG TCG ACT AGT AC 3' 5' GTA ATG CAC ACTCCA TTG GC 3' 5' GTA ATG CAC ACTCCA TTG GC 3' 5' GTA ATG CAC ACTCCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG 3' 5' GGG CTC AGC TGG AAT TCC 3' 5' GGA ATT CCA CTC AGT AGT AC 3' 5' GTA ATG CAC ACTCCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG 3' 5' GGG CTC AGC TGG AAT TCC 3' 5' GTA ATG CAC ACT CCA TTG 3' 5' GTA ATG CAC ACT CCA TTG 3' 5' GTA ATG CAC ACT CCA TTG 3' 5' GGG CTC AGC TGG AAT TCC 3' 5' GTG GGA TTC CA GTG AGT CGC CTA CC 3' 5' GTG GGA TTC CCA TTG ACC 3' 5' GTG GGA TTC CAC TGG AAT TCC 3' 5' GGC CTC AGC TGG AAT TCC 3' 5' GGC CTC AGC TGG AAT TCC 3' 5' GGC CTC AGC TGG AAT TCC 3' 5' GGA ATT CCA GCT GAG CGC 3' 5' GTG GGA TCC CCA TGA CGA CCG CGT CCA CC 3' 5' GTG GGA TCC CCA TGA CGA CGG CGT CCA CC 3' 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3'	5' GAC CCC CAT TTG TGT GAC 3'	SEQ ID NO:12
5' AGC CGA CAG CGA TTT CTA GGA TAG 3' SEQ.ID.NO:15 5' GTT CTT CAA AGC CAC ATC ATC GCG GTC 3' SEQ.ID.NO:16 5' GCT TTC ATT ATC ACT GTC TCC CAG GGT G 3' SEQ.ID.NO:17 5' CAG ACG TTC TTC GCC GAG AGT CGT 3' SEQ.ID.NO:18 5' CAG ACG TTC TTC GCC GAG AGT CGT 3' SEQ.ID.NO:19 5' CAT TTC GGG GAT TCG GGG GA 3' SEQ.ID.NO:20 5' GGG GGA CGG AAC CCG GCG CT 3' SEQ.ID.NO:21 5' CCC TCT ACA CTT ATC ATC TTC 3' SEQ.ID.NO:22 5' CTA TCC TAG AAA TCG CTG TCG GCT 3' SEQ.ID.NO:23 5' GTC ACT ACT GGA ATT CCC TTC TCC 3' SEQ.ID.NO:24 5' GGA GAA GGG AAT TCC AGT AGT GAC 3' SEQ.ID.NO:25 5' GGA AAT CGC TGT CGC CTA ACC 3' SEQ.ID.NO:26 5' GGT TAG GCG ACA GCG ATT TCC 3' SEQ.ID.NO:27 5' GGC CAC GCG TCG ACT AGT AGT AGT SCO.25 5' GTA ATG CAC ACTCCA TTG GC 3' SEQ.ID.NO:28 5' GTA ATG CAC ACT CCA TTG 3' SEQ.ID.NO:30 5' GCG CTC AGC TGG AAT TCC 3' SEQ.ID.NO:31 5' GGA ATT CCA GCT GAG CGC 3' SEQ.ID.NO:32 5' GTG GGA TCC CCA TGA CGA CCG CGT CCA CC 3' SEQ.ID.NO:33 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' SEQ.ID.NO:33 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' SEQ.ID.NO:34 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' SEQ.ID.NO:35	5' CGA CGA CTC CTG GAG CCC G 3'	SEQ ID NO:13
5' GTT CTT CAA AGC CAC ATC ATC GCG GTC 3' 5' GCT TTC ATT ATC ACT GTC TCC CAG GGT G 3' 5' CAG ACG TTC TTC GCC GAG AGT CGT 3' 5' CAG ACG TTC TTC GCC GAG AGT CGT 3' 5' CAG ACG TTC TTC GCC GAG AGT CGT 3' 5' CAT TTC GGC GAG AGT CGT CGG 3' 5' CAT TTC GGG GAT TCG GGG GA 3' 5' CAT TTC GGG GAT TCG GGG GA 3' 5' GGG GGA CGG AAC CCG GCG CT 3' 5' CCC TCT ACA CTT ATC ATC TTC 3' 5' CTA TCC TAG AAA TCG CTG TCG GCT 3' 5' GTC ACT ACT GGA ATT CCC TTC TCC 3' 5' GGA GAA GGG AAT TCC AGT AGT GAC 3' 5' GGA AAT CGC TGT CGC CTA ACC 3' 5' GGT TAG GCG ACA GCG ATT TCC 3' 5' GGC CAC GCG TCG ACT AGT AC 3' 5' GTA ATG CAC ACTCCA TTG GC 3' 5' GTA ATG CAC ACTCCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG 3' 5' GGA CTC AGC TGG AAT TCC 3' 5' GTA ATG CAC ACT CCA TTG 3' 5' GGA ATT CCA GCT GAG CGC 3' 5' GTG GGA TCC CCA TGA CGC CGT CCA CC 3' 5' GTG GGA TCC CCA TGA CGC CGT CCA CC 3' 5' GTG GGA TCC CCA TGA CGC CGT CCA CC 3' 5' GTG GGA TCC CCA TGA CGC CGT CCA CC 3' 5' GTG GGA TCC CCA TGA CGC CGT CCA CC 3' 5' GTG GGA TCC CCA TGA CGA CCG CGT CCA CC 3' 5' GTG GGA TCC CCA TGA CGA CCG CGT CCA CC 3' 5' GTG GGA TCC CCA TGA CGA CCG CGT CCA CC 3' 5' GTG GGA TCC CCA TGA CGA CCG CGT CCA CC 3' 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3'	5' Biotin-TTG ACA CCA GAC CAA CTC GTA ATG 3'	SEQ ID NO:14
5' GCT TTC ATT ATC ACT GTC TCC CAG GGT G 3' 5' CAG ACG TTC TTC GCC GAG AGT CGT 3' 5' CAG ACG TTC TTC GCC GAG AGT CGT 3' 5' CAG ACG TTC TTC GCC GAG AGT CGT CGG 3' 5' CAT TTC GGG GAT TCG GGG GA 3' 5' CAT TTC GGG GAT TCG GGG GA 3' 5' GGG GGA CGG AAC CCG GCG CT 3' 5' CCC TCT ACA CTT ATC ATC TTC 3' 5' CTA TCC TAG AAA TCG CTG TCG GCT 3' 5' GTC ACT ACT GGA ATT CCC TTC TCC 3' 5' GGA GAA GGG AAT TCC AGT AGT GAC 3' 5' GGA AAT CGC TGT CGC CTA ACC 3' 5' GGT TAG GCG ACA GCG ATT TCC 3' 5' GGC CAC GCG TCG ACT AGT AC 3' 5' GTA ATG CAC ACTCCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG 3' 5' GTA ATG CAC ACT CCA TTG 3' 5' GGA ATT CCA GCT GACT AGT ACC 3' 5' GTA ATG CAC ACT CCA TTG 3' 5' GTA ATG CAC ACT CCA TTG 3' 5' GGA ATT CCA GCT GAG CGC 3' 5' GTA GGA TCC CCA TGA CGA CCG CGT CCA CC 3' 5' GTA GGA TCC CCA TGA CGA CCG CGT CCA CC 3' 5' GTA GGA TCC CCA TGA CGA CCG CGT CCA CC 3' 5' GTA GGA TCC CCA TGA CGA CCG CGT CCA CC 3' 5' GTA GGA TCC CCA TGA CGA CCG CGT CCA CC 3' 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3'	5' AGC CGA CAG CGA TTT CTA GGA TAG 3'	SEQ ID NO:15
5' CAG ACG TTC TTC GCC GAG AGT CGT 3' 5' CAG ACG TTC TTC GCC GAG AGT CGT CGG 3' 5' CAT TTC GGG GAT TCG GGG GA 3' 5' CAT TTC GGG GAT TCG GGG GA 3' 5' GGG GGA CGG AAC CCG GCG CT 3' 5' CCC TCT ACA CTT ATC ATC TTC 3' 5' CTA TCC TAG AAA TCG CTG TCG GCT 3' 5' GTC ACT ACT GGA ATT CCC TTC TCC 3' 5' GGA GAA GGG AAT CCC TTC TCC 3' 5' GGA GAA GGG AAT TCC AGT AGT GAC 3' 5' GGA AAT CGC TGT CGC CTA ACC 3' 5' GGC CAC GCG TCG ACT AGT AC 3' 5' GGC CAC GCG TCG ACT AGT AC 3' 5' GTA ATG CAC ACT CCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG 3' 5' GTA ATG CAC ACT CCA TTG 3' 5' GGG CTC AGC TGG AAT TCC 3' 5' GGG CTC AGC TGG AAT TCC 3' 5' GTG GGA TCC CCA TGG CGC 3' 5' GTG GGA TCC CCA TGA CGC CGT CCA CC 3' 5' GTG GGA TCC CCA TGA CGA CCG CGT CCA CC 3' 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3'	5' GTT CTT CAA AGC CAC ATC ATC GCG GTC 3'	SEQ ID NO:16
5' CAG ACG TTC TTC GCC GAG AGT CGT CGG 3' 5' CAT TTC GGG GAT TCG GGG GA 3' 5' GGG GGA CGG AAC CCG GCG CT 3' 5' CCC TCT ACA CTT ATC ATC TTC 3' 5' CTA TCC TAG AAA TCG CTG TCG GCT 3' 5' GTC ACT ACT GGA ATT CCC TTC TCC 3' 5' GGA GAA GGG AAT TCC AGT AGT GAC 3' 5' GGA AAT CGC TGT CGC CTA ACC 3' 5' GGT TAG GCG ACA GCG ATT TCC 3' 5' GGC CAC GCG TCG ACT AGT AC 3' 5' GTA ATG CAC ACTCCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG 3' 5' GTA ATG CAC ACT CCA TTG 3' 5' GGA ATT CCA GCT GAG CGC GAT TTC 3' 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT TAA GCC GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5EQ ID NO:34 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5EQ ID NO:35	5' GCT TTC ATT ATC ACT GTC TCC CAG GGT G 3'	SEQ ID NO:17
5' CAT TTC GGG GAT TCG GGG GA 3' 5' GGG GGA CGG AAC CCG GCG CT 3' 5' CCC TCT ACA CTT ATC ATC TTC 3' 5' CTA TCC TAG AAA TCG CTG TCG GCT 3' 5' GTC ACT ACT GGA ATT CCC TTC TCC 3' 5' GGA GAA GGG AAT TCC AGT AGT GAC 3' 5' GGA GAA GGG AAT TCC AGT AGT GAC 3' 5' GGT TAG GCG ACA GCG ATT TCC 3' 5' GGC CAC GCG TCG ACT AGT AC 3' 5' GTA ATG CAC ACTCCA TTG GC 3' 5' GTA ATG CAC ACTCCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG 3' 5' GCG CTC AGC TGG AAT TCC 3' 5' GTA ATG CAC ACT CCA TTG 3' 5' GCG CTC AGC TGG AAT TCC 3' 5' GTA ATG CAC ACT CCA TTG 3' 5' GCG CTC AGC TGG AAT TCC 3' 5' GCG CTC AGC TGG AAT TCC 3' 5' GCG CTC AGC TGG ACT CCA TTG 3' 5' GCG CTC AGC TGG CGC 3' 5' GTG GGA TCC CCA TGA CGA CCG CGT CCA CC 3' 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5 EQ ID NO:34 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5 EQ ID NO:35	5' CAG ACG TTC TTC GCC GAG AGT CGT 3'	SEQ ID NO:18
5' GGG GGA CGG AAC CCG GCG CT 3' 5' CCC TCT ACA CTT ATC ATC TTC 3' 5' CTA TCC TAG AAA TCG CTG TCG GCT 3' 5' GTC ACT ACT GGA ATT CCC TTC TCC 3' 5' GGA GAA GGG AAT TCC AGT AGT GAC 3' 5' GGA AAT CGC TGT CGC CTA ACC 3' 5' GGA AAT CGC TGT CGC CTA ACC 3' 5' GGC CAC GCG TCG ACT AGT AC 3' 5' GGC CAC GCG TCG ACT AGT AC 3' 5' GTA ATG CAC ACTCCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG 3' 5' GCG CTC AGC TGG AAT TCC 3' 5' GCG CTC AGC TGG AAT TCC 3' 5' GTA ATG CAC ACT CCA TTG 3' 5' GCG CTC AGC TGG AAT TCC 3' 5' GCG CTC AGC TGG CGC 3' 5' GCG CTC AGC TGA CGA CCG CGT CCA CC 3' 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3'	5' CAG ACG TTC TTC GCC GAG AGT CGT CGG 3'	SEQ ID NO:19
5' CCC TCT ACA CTT ATC ATC TTC 3' 5' CTA TCC TAG AAA TCG CTG TCG GCT 3' 5' GTC ACT ACT GGA ATT CCC TTC TCC 3' 5' GGA GAA GGG AAT TCC AGT AGT GAC 3' 5' GGA GAA GGG AAT TCC AGT AGT GAC 3' 5' GGA AAT CGC TGT CGC CTA ACC 3' 5' GGT TAG GCG ACA GCG ATT TCC 3' 5' GGC CAC GCG TCG ACT AGT AC 3' 5' GTA ATG CAC ACTCCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG 3' 5' GCG CTC AGC TGG AAT TCC 3' 5' GCG CTC AGC TGG CGC 3' 5' GCG CTC AGC TGA CGA CCG CGT CCA CC 3' 5' GAC TCC AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' SEQ.ID.NO:34 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' SEQ.ID.NO:35	5' CAT TTC GGG GAT TCG GGG GA 3'	SEQ ID NO:20
5' CTA TCC TAG AAA TCG CTG TCG GCT 3' 5' GTC ACT ACT GGA ATT CCC TTC TCC 3' 5' GGA GAA GGG AAT TCC AGT AGT GAC 3' 5' GGA AAT CGC TGT CGC CTA ACC 3' 5' GGA AAT CGC TGT CGC CTA ACC 3' 5' GGT TAG GCG ACA GCG ATT TCC 3' 5' GGC CAC GCG TCG ACT AGT AC 3' 5' GTA ATG CAC ACTCCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG 3' 5' GCG CTC AGC TGG AAT TCC 3' 5' GGA ATT CCA GCT GAG CGC 3' 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' SEQ ID NO:34 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' SEQ ID NO:35	5' GGG GGA CGG AAC CCG GCG CT 3'	SEQ ID NO:21
5' GTC ACT ACT GGA ATT CCC TTC TCC 3' 5' GGA GAA GGG AAT TCC AGT AGT GAC 3' 5' GGA AAT CGC TGT CGC CTA ACC 3' 5' GGT TAG GCG ACA GCG ATT TCC 3' 5' GGC CAC GCG TCG ACT AGT AC 3' 5' GTA ATG CAC ACT CCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG 3' 5' GCG CTC AGC TGG AAT TCC 3' 5' GGA ATT CCA GCT GAG CGC 3' 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' SEQ ID NO:34 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' SEQ ID NO:35	5' CCC TCT ACA CTT ATC ATC TTC 3'	SEQ ID NO:22
5' GGA GAA GGG AAT TCC AGT AGT GAC 3' 5' GGA AAT CGC TGT CGC CTA ACC 3' 5' GGT TAG GCG ACA GCG ATT TCC 3' 5' GGC CAC GCG TCG ACT AGT AC 3' 5' GTA ATG CAC ACTCCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG 3' 5' GCG CTC AGC TGG AAT TCC 3' 5' GGA ATT CCA GCT GAG CGC 3' 5' GGA ATT CCA GCT GAG CGC 3' 5' GGA ATT CCA GCT GAG CGC 3' 5' GTG GGA TCC CCA TGA CGA CCG CGT CCA CC 3' 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' SEQ ID NO:35 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' SEQ ID NO:35	5' CTA TCC TAG AAA TCG CTG TCG GCT 3'	SEQ_ID_NO:23
5' GGA AAT CGC TGT CGC CTA ACC 3' 5' GGT TAG GCG ACA GCG ATT TCC 3' 5' GGC CAC GCG TCG ACT AGT AC 3' 5' GTA ATG CAC ACTCCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG 3' 5' GCG CTC AGC TGG AAT TCC 3' 5' GCG CTC AGC TGG AAT TCC 3' 5' GGA ATT CCA GCT GAG CGC 3' 5' GTG GGA TCC CCA TGA CGA CCG CGT CCA CC 3' 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' SEQ ID NO:31 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' SEQ ID NO:35	5' GTC ACT ACT GGA ATT CCC TTC TCC 3'	SEQ ID NO:24
5' GGT TAG GCG ACA GCG ATT TCC 3' 5' GGC CAC GCG TCG ACT AGT AC 3' 5' GTA ATG CAC ACTCCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG 3' 5' GCG CTC AGC TGG AAT TCC 3' 5' GGA ATT CCA GCT GAG CGC 3' 5' GTG GGA TCC CCA TGA CGA CCG CGT CCA CC 3' 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' SEQ ID NO:32 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' SEQ ID NO:35	5' GGA GAA GGG AAT TCC AGT AGT GAC 3'	SEQ ID NO:25
5' GGC CAC GCG TCG ACT AGT AC 3' 5' GTA ATG CAC ACTCCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG 3' 5' GCG CTC AGC TGG AAT TCC 3' 5' GGA ATT CCA GCT GAG CGC 3' 5' GTG GGA TCC CCA TGA CGA CCG CGT CCA CC 3' 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' SEQ ID NO:32 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' SEQ ID NO:35	5' GGA AAT CGC TGT CGC CTA ACC 3'	SEQ ID NO:26
5' GTA ATG CAC ACTCCA TTG GC 3' 5' GTA ATG CAC ACT CCA TTG 3' 5' GCG CTC AGC TGG AAT TCC 3' 5' GGA ATT CCA GCT GAG CGC 3' 5' GTG GGA TCC CCA TGA CGA CCG CGT CCA CC 3' 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' SEQ ID NO:32 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' SEQ ID NO:35	5' GGT TAG GCG ACA GCG ATT TCC 3'	SEQ ID NO:27
5' GTA ATG CAC ACT CCA TTG 3' 5' GCG CTC AGC TGG AAT TCC 3' 5' GGA ATT CCA GCT GAG CGC 3' 5' GTG GGA TCC CCA TGA CGA CCG CGT CCA CC 3' 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' SEQ ID NO:35	5' GGC CAC GCG TCG ACT AGT AC 3'	SEQ ID NO:28
5' GCG CTC AGC TGG AAT TCC 3' 5' GGA ATT CCA GCT GAG CGC 3' 5' GTG GGA TCC CCA TGA CGA CCG CGT CCA CC 3' 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' SEQ ID NO:35	5' GTA ATG CAC ACTCCA TTG GC 3'	SEQ ID NO:29
5' GGA ATT CCA GCT GAG CGC 3' 5' GTG GGA TCC CCA TGA CGA CCG CGT CCA CC 3' 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' SEQ ID NO:35	5' GTA ATG CAC ACT CCA TTG 3'	SEQ ID NO:30
5' GTG GGA TCC CCA TGA CGA CCG CGT CCA CC 3' 5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' SEQ ID NO:35	5' GCG CTC AGC TGG AAT TCC 3'	SEQ ID NO:31
5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3' 5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' SEQ ID NO:35	5' GGA ATT CCA GCT GAG CGC 3'	SEQ ID NO:32
5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3' SEQ ID NO:35	5' GTG GGA TCC CCA TGA CGA CCG CGT CCA CC 3'	SEQ ID NO:33
	5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3'	SEQ ID NO:34
5' CCC GCT CGA GTC AGG GTG ACC GAA AAA TCA G 3' SEQ.ID.NO:36	5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3'	SEQ ID NO:35
	5' CCC GCT CGA GTC AGG GTG ACC GAA AAA TCA G 3'	SEQ ID NO:36

The two paragraphs beginning at line 6 on page 16 and ending at line 13 of page 16 have been amended as follows:

Fig. 1 shows the nucleic acid sequence (SEO ID NO:1) of clone T16 isolated from T47D breast cancer cDNA library.

Initiation and termination codons of the open reading frame are indicated by dark bars;

Fig. 2A shows a comparison of the nucleic acid sequences (upper sequence) (SEO ID NO:2) of clone 4.7 isolated from a placenta cDNA library exhibiting normal human FTH, and the sequences (lower sequence) of clone T16 (SEO ID NO:1) isolated from human breast cancer T47D cDNA library. Initiation and termination codons of the open reading frame are marked by dark boxes;

The three paragraphs beginning at line 17 of page 16 and ending at line 25 of page 16 have been amended as follows:

- Fig. 3 shows a comparison of sequence homology between cDNA clone T16 (residues 463-671 of SEO ID NO:1) and human mitochondrial cytochrone oxidase I DNA (SEO ID NO:3);
- Fig. 4 shows a comparison of nucleic acid sequences between placental cDNA obtained by PCR amplification using T16 specific primers (upper sequence) (residues 24-822 of SEO ID NO:1) and T16 cDNA sequence obtained from the T16 cDNA clone (lower sequence) (SEO ID NO:4). Identical nucleic acid sequences are indicated by a dotted line. Initiation and termination codons are indicated by a dark bar;
- Fig. 5 shows the nucleic acid sequence and deduced amino acid sequence (SEQ ID NO:5) of the cDNA of OFF1;

The two paragraphs beginning at line 4 of page 17 and ending at line 6 of page 17 have been amended as follows:

Fig. 7 shows the sequence of clone T16 (SEO ID NO:1). pPrimers used for PCR are indicated in the above sequence;

Fig. 8 shows the restriction enzyme map sequence of clone T16 (SEO ID NO:1);

Table 1 on page 19 has been amended as follows:

Table 1
List of Primers

	Name	#MR	Sequence	SEQ_ID		
			•	NO:		
	1060F	24	5' GGT GGC GAC GAC TCC TGG AGC CCG 3'	6	75%	
	1061R	24	5' TTG ACA CCA GAC CAA CTG GTA ATG 3'	2	45.80%	
	17F	27	5' GAC CGC GAT GAT GTG GCT TTG AAG AAC 3'	8	52%	27618
	X1.1F	24	5' GAT AGG ATC TTT AGC GAC AGC CGA 3'	9	50%	24880
	X.1.1R	24	5' ATG GCG GCC TCT GAG TCC TGG TGG 3'	10	67%	
	2.1 F	24	5' CGG GCT GAA TGC AAT GGA GTG TGC 3'	11	58%	
n" III	3.4 F	18	5' GAC CCC CAT TTG TGT GAC 3'	12	55.50%	
H	1060F/S	19	5' CGA CGA CTC CTG GAG CCC G 3'	13	73.70%	
T	1061r/Bio	24	5' Biotin-TTG ACA CCA GAC CAA CTC GTA ATG 3'	14	45.80%	
핔	16X.1R	24	5' AGC CGA CAG CGA TTT CTA GGA TAG 3'	15	50%	24879
E E	17R	27	5' GTT CTT CAA AGC CAC ATC ATC GCG GTC 3'	16	52%	27385
18	3'COD R	28	5' GCT TTC ATT ATC ACT GTC TCC CAG GGT G 3'	17	50%	28313
	5' NCF	24	5' CAG ACG TTC TTC GCC GAG AGT CGT 3'	1.8	58%	24870
Д	4869	27	5' CAG ACG TTC TTC GCC GAG AGT CGT CGG 3'	19	63%	
14	NFG	20	5' CAT TTC GGG GAT TCG GGG GA 3'	20	60%	
	NFGP-2	20	5' GGG GGA CGG AAC CCG GCG CT 3'	21	80%	201880
=4	767-F	21	5' CCC TCT ACA CTT ATC ATC TTC 3'	22	43%	211616
	16-F	24	5' CTA TCC TAG AAA TCG CTG TCG GCT 3'	23	50%	241173
	ECO-F	24	5' GTC ACT ACT GGA ATT CCC TTC TCC 3'	24	50%	24960
	ECO-R	24	5' GGA GAA GGG AAT TCC AGT AGT GAC 3'	25	50%	24961
	SPF	21	5' GGA AAT CGC TGT CGC CTA ACC 3'	26	57%	211667
	SPR	21	5' GGT TAG GCG ACA GCG ATT TCC 3'	27	57%	211668
	AUAP	20	5' GGC CAC GCG TCG ACT AGT AC 3'	28	65%	202738
	NC-F	20	5' GTA ATG CAC ACTCCA TTG GC 3'	29	50%	203814
	SNC-F	18	5' GTA ATG CAC ACT CCA TTG 3'	3.0	44%	181897
	BNC-F	18	5' GCG CTC AGC TGG AAT TCC 3'	31	55.50%	181898
	BNC-R	18	5' GGA ATT CCA GCT GAG CGC 3'	32	61.10%	181905
	pGEX-F	29	5' GTG GGA TCC CCA TGA CGA CCG CGT CCA CC3'	33	67%	29391
	pGEX-R1	27	5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3'	34	51.85%	27578
	pGEX-R2	29	5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3'	35	51.70%	29396
	pGEX-R3	31	5' CCCGCTCGAGTCAGGGTGACCGAAAAATCAG 3'	36	58%	31277

The paragraph beginning at line 6 on page 27 has been amended as follows:

The expression vector (pGEX-5X-1) used for gene fusion construction was the GST Gene Fusion System (Pharmacia). The OFF1 coding region (designated as "FL", full-length) of about 0.5 kb was prepared by PCR with the following 5' end primer:

5' GTGGGATCCCCATGACGACCGCGTCCA (1-27 of SEQ ID NO:33), in order BamHI

to add a BamHI site 1 base upstream from the start codon ATG and with the 3^\prime end primer

5' CCCG CTCGAG TCA GGG TGA CCG AAA AAT CAG 3' (SEO ID NO:36) in Xho1

order to add an Xhol site after the stop codon TAA using the PCR kit (Perkin-Elmer/Centus).

5" TTGACACCAG	ACCAACTGGT	AATGGTAGCG	ACCGGCGCTC	AGCTGGZATT	AA CC J AAAATG
TAATGCACAC	TCCATTGECAT	TCAGCCCGCC	TCTCCTTAGT	CGCCGCCATG	ACGACCGCGT
CCACÇTCGCA	GGTGCGCCAG	AACTACCACC	AGGACTCAGA	GGCCGCCATC	A.A.CCGCCAGA
TCAACCTGGA	GCTCTACGCC	TCCTACGTTT	ACCTGTCCAT	GTCTTACTAC	TTTGACCGCG
ATGATGTGGC	TTTGAAGAAC	TTTGCCAAAT	ACTITCTICA	CCAATCTCAT	GACGAGAGGG
AACATGCTGA	GAAACTGATG	AAGCTGCAGA	ACCAACGAGG	TGGCCGAATC	TTCCTTCAGG
ATATCAAGAA.	ACCAGACTGT	GATGACTGGG	AGAGCGGGCT	GAATGCAATG	GAGTGTGCAT
TACATTTGGA	AAAAAATGTG .	AATCAGTCAC	TACTGGAATT	CCCTTCTCCT	ATCTCTCCCA
GTCCTAGCTG	CTGGCATCAC	TATACTACTA	ACAGACCGCA	ACCTCAACAC	CACCTTCTTC
GACCCCCCCG	GAGGAAGAGA	CCCCATTCTA	TACCAACACC	TATTCTGATT	TITCGGTCAC
COTGAAGTTT	ATATTCTTAT	CCTACCAGGC	TTCGGAATAA	TCTCCCATAT	TGTAACTTAC
TACTCCGGAA	ATCGCTGTCG	CCTAACCGCT	AACATTACTG	CAGGCCACCT	ACTCATGCAC
CTAATTGGAA	GCGCCACCCT	AGCAATATCA	ACCATTAACC	TTCCCTCTAC	ACTTATCATC
TTCACAATTC	TAATTCTACT	GACTATCCTA	GAAATCGCTG	TCGCCTTAAT	CCAAGCCTAC
	TTCTACTACA	CCTCTACCT G	&CACGACAAC A	- ∦ CATAAAAAAA	A# 3"

Fig. 1

2/15 CLONE 047

GGGGACGGAACCCGG

Fig. 2A

CGCTCGTTCCCCACCCGGCCGGCCGCCCATAGCCAGCCCTCCGTCAC CLONE T 16 .. TTGACACC

CTCTTCACCGCACCCTCGGACTGCCCCAAGGCCCCCGCCGCCGCTCC AGACCAACTGGTAATGGTAGCGACCGGCGCTCAGCTGGAATTCCAAAA

AGCGCCGCAGCCACCGCCGCCGCCGCCTCTCCTTAGTCGCCGCCAATGTAATGCACACTCCATTGCATTCAGCCCGCCTCTCCTTAGTCGCCGCC

A	TG	ACG	ACC	GCG	тсс	ACC	TCG	CAG	GTG	CGC	CAG
A	TG	ACG	ACC	GCG -	TCC	ACC	TCG	CAG	GTG .	CGC _.	CAG
2	AC.	TAC	CAC	CAG	GAC	TCA	GAG	GCC	GCC	ATC	AAC
	AC .	TAC	CAC	CAG	GAC	TCA	GAG	GCC	GCC	ATC	AAC
(CGC	CAG	ATC	AAC	CTG	GAG	CTC	TAC	GCC	TCC	TAC
	CGC	CAG ·	ATC	AAC	CTG.	GAG	CTC	TAC	GCC	TCC	TAC
	GTT	TAC	CTG	TCC	ATG	TCT	TAC	TAC	TTT	GAC	CGC
	GTT	TAC.	CTG	TCC	ATG	TCT	TAC	TAC	111	GAC _.	CGC
	GAT	GAT	GTG	GCT	TTG	AAG	AAC	TTT	GCC	AAA	TAC
	GAT	GAT	GTG	GCT	TTG	AAG	AAC	111	GCC.	AAA	TAC
	111	CTT	CAC	CAA	TCT	CAŤ	GAG	GAG	AGG	GAA	CAT
	П	CTT	CAC	CAA	TCT	CAT	GAG	GAG	AGG	GAA	CAT
	GCT	GAG	AAA	CTG	ATG	AAG	CTG	CAG	AAC	CAA	CGA
	GCT	GAG	AAÀ	СТĠ	ATG	AAG	CTG	CAG	AAC	CAA	CGA
	GGT	GGC	CGA	ATC	TTC	CTT	CAG	GAT-	ATC	AAG	AAA
	GGT	GGC	ÇGA	ATC	TTC	CTT	CAG	GAT	ATC	AAG	AAA,
	CCA	GAC	TGT	GAT	GAC	TGG	GAG	AGC	GGG	CTG	AAT
	CCA	. GAC	TGT	GAT	GAC	TGG	GAG	AGC	GGG	CTG	AAT
	CC^-	ATG	GAG	TGT	GCA	TTA	CAT	TTG	GAA		AAT
	GCA GCA	ATG	GAG		GCA		CAT	TTG	GAA	AAA	AAT
			010	TCA	СТА	CTG	GAA	CTG	CAC	AAA	CTG
	GTG	TAA TAA	CAG CAG					TTC	CCT	TCT	CCT
	GTG	AA!	OAG.	, , , , ,		-					
	GCC	ACT	GAC	: AAA	AAT	GAC					
	ATC	TCT		AGT	CCT	AGC	TGC	TGC	G CAT	CAC	, 101

3/15

									-	-
 -	A. 1.1	GAG	ACA	CAT	TAC	CTG	AAT	GAG	CAG	GTG
TTC		AAC	AGA	CCG	CAA -	CCT	CAA	CAC	CAC	CTT
ACT	ACT	AAC	AGA	- \ \\\			-			
3 4 4	GCC	-ATC	AAA	GAA	TTG	GGT	GAC	CAC	GTG	ACC
AAA		CCC	CGC	CGG.	AGG	AAG	AGA	CCC	CAT	TCT
CTT	CGA		<u></u>							• -
AAC	πg	CGC	AAG	ATG	GGA	GCG	ccc	GAA	TCT	GGC
ATA	CCA	ACA	CCT	ATT	CTG	ATT	TT	CGG	TCA	CCC
AIA		707								
TTG	GCG	GAA	TAT	CTC	TTT	GAC	AAG	CAC	ACC	CTG
TGA			CTTATC	CTACCA	GGCTTC	GGAAT	AATCTC	CCATAT	Τ	
10/1	1.1.5.1.1				•					
GGA	GAC	AGT	GAT	AAT	GAA	AGC	TAA	GCCT	CGGGC	TAATT
GTAA	CTTACT	ACTCC	SGAAAT	CGCTGT	CGCCTA	ACCGC	TAACAT	TACTGO	<u> </u>	
TCCC	ATAGCO	CGTGGG	GTGAC	TCCCT	GGTCAC	CAAGG	CAGTG	CATGCA	Ţ	
AGGC	CACCTA	ACTCAT	GCACCT	AATTGG	BAAGCG	CCACC	CTAGCA	ATATCA		
GCAT	GTTGG	GGTTTC	CTTTAC	стттс	TATAAG	TTGTA	CAAAA	CATCCA	С	
ACCA	TTAACC	TTCCC	TCTACA	STTATC	ATCTTC	ACAATT	CTAATT	CTACTO	}	<u> </u>
								-		
TTAA	GTTCTT	TGATTI	TGTACCA	ATTCCT	CAAATA	AAAGAA	ATTTGG	TACCC	4	
ACTA	TCCTAC	BAAATC	GCTGTC	GCCTTA	ATCCA/	AGCCTA	CGTTT	CACACT	<u> </u>	
							. • .			•
AAAA	AAAA				C				•	•
			00±00*	CCACA	AMACATA	ΔΔΔΔΔ	AA			

Fig. 2A Cont.

7/15
TTGACACCAGACCAACTGGTAATGGTAGCGACCGGCGCTCAGCTGGAATTCCAAAAAATGT

AATGCACACTCCATTGCATTCAGCCCGCCTCTCCTTAGTCGCCGCC

701100					•					
met	thr	thr	ala	ser	thr	ser	gIn	val	arg	gin
ATG	ACG	ACC	GCG	TCC	ACC	TCG	CAG ⁻	GTG	CGC	CAG
asn	tyr	his	gln	asp	ser	glu	ala	ala	ile	asn
AAC	TAC	CAC	CAG	GAC	TCA	GAG	GCC	GCC	ATČ	AAC
arg CGC	gin CAG	île ATC	asn AAC	leu _. CTG	glu GAG	leu CTC	tyr TAC	ala GCC	ser TCC	tyr TAC
val	tyr	leu	ser	met	ser	tyr	tyr	phe	asp	arg
GTT	TAC	CTG	TCC	ATG	TCT	TAC	TAC	TTT	GAC	CGC
asp	asp	val	ata	leu	lys	asn	phe	ala	lys	tyr
GAT	GAT	GTG	GCT	TTG	AAG	AAC	TTT	GCC	AAA	TAC
phe	leu	his	gln	ser	his	glu	glu	arg	gin	his
TTT	CTT	CAC	CAA	TCT	CAT	GAG	GAG	AGG	GAA	CAT
ala	glu	lys	leu	met	lys	leu	gln	asn	gin	arg
GCT	GAG	AAA	CTG	ATG	AAG	CTG	CAG	AAC	CAA	CGA
gly	gły	arg	īle	phe	leu	gin	asp	ije	lys	-AAA
GGT	GGC	CGA	ATC	TTC	CTT	CAG	GAT	ATC	AAG	
pro	asp	cys	asp	asp	trp	glu	ser	gly	leu	asn
CCA	GAC	TGT	GAT	GAC	TGG	GAG	AGC	GGG	CTG	AAT
ala	met	glu	cys	ala	leu	his	leu	glu	lys	asn
GCA	ATG	GAG	TGT	GCA	TTA	CAT	TTG	GAA	AAA	AAT
val	asn	gin	ser	leu	leu	glu	phe	pro	ser	pro
GTG	AAT	CAG	TCA	CTA	CTG	GAA	TTC	CCT	TCT	CCT
ile	ser	pro	ser	pro	ser	cys	trp	his	his	thr
ATC	TCT	CCC		CCT	AGC	TGC	TGG	CAT	CAC	TAT
thr	thr	asn AAC	arg AGA	pro CCG	glu CAA	pro CCT	gln CAA	his CAC	his CAC	leu CTT
leu	arg	pro	arg	arg	arg	lys	arg AGA	pro	his CAT	ser TCT
ile	pro	thr	pro	ile	leu CTG	ile	, phe	arg	ser	рго
· ATA	CCA	ACA	CCT	ATT	CIG					

TGA AGTITATATTCTTATCCTACCAGGCTTCGGAATAATCTCCCATATTGTAACTTAC

TACTCCGGAAATCGCTGTCGCCTAACCGCTAACATTACTGCAGGCCACCTACTCATGCAC

CTAATTGGAAGCGCCACCCTAGCAATATCAACCATTAACCTTCCCTCTACACTTATCATC

TTCACAATTCTAATTCTACTGACTATCCTAGAAATCGCTGTCGCCTTAATCCAAGCCTAC

GTTTCACACTTTEETAGECTERAGEA CTAGTAA GCCTCTACCTGCACGACAA CASATAAAAAAAA

10/15

[:]	1061 TGACACCAG	ACCAACTGGT	<u>AATG</u> GTAGCG	BNC ACCGGCGCTC	AGCTGGAATTI	<u>ETALLALAD</u>
ī	NCS AATGCACAC	TCCATTGCAT	TCAGCCCGCC	TCTCCTTAGT	CGCCGCCATG	ACGACCGCGT
c	CACCTCGCA	GGTGCGCCAG	AACTACCACC	. X1 AGGACTCAGAI	<u>GGCCGCCAT</u> G	AACCGCCAGA
7	CAACCTGGA	GCTCTACGCC	TCCTACGTTT	ACCTGTCCAT	GTCTTACTAC	17 TTTGACCGCG
٠ <u>.</u> و	17 ATGATGTGGQ	DAAGAAGTT	TTTGCCAAAT	ACTTTCTTCA	CCAATCTCAT	GAGGAGAGGG
	AACATGCTGA	GAAACTGATG	AAGCTGCAGA	ACCAACGAGG	TGGCCGAATC	TTCCTTCAGG
	ATATCAAGAA	ACCAGACTGT	GATGACTGGG	AGAGCGGGCT	2.1 GAATGCAATG	GAGTGTGCAT
	TACATTTGGA	AAAAAATGTG	AATCAGTCAG	ECOF TACTGGAATT	ECCTTCTCGT	ATCTCTCCCA
	GTCCTAGCTG	CTGGCATCAC	TATACTACTA	ACAGACCGCA	ACCTCAACAC	CACCTTCTTC
	GACCCCGCCG	GAGGAAGAGA	CCCCATTCTA	TACCAACACC	TATTCTGATT	TTTCGGTCAC
	CCTGAAGTTT	ATATTCTTAT	CCTACCAGGC	TTCGGAATAA	TCTCCCATAT	TGTAACTTAC
	TACTCCGGAA	SPF ATCGCTGTCG	CCTAACGGCT	AACATTACTG	CAGGCCACCT	ACTCATGCAC
	CTAATTGGAA	728 GCGCCACCCT	AGCAATATCA	ACCATTAACC	TTCCCTCTAC	767 ACTTATCATO
	161	MAATTCTACT	GACTATCCTA	16 GAAATCGCTG	TCGCCTTAAT	CCAAGCCTAC
	GTTTTCACAC	TTCTAGTAAG	¢CCTCTACCTG	G CACGACAAC	*CATAAAAA	A A .

Fig. 7

PCT/IL99/00485 WO 00/15788 11/15 CCAAAAAATG AGCTGGAATT ACCGGCGCTC AATGGTAGCG ACCAACTGGT TTGACACCAG ACGACCGCGT CCCCCCX TCTCCTTAGT TCAGCECGCE TCCATTGCAT TAATGCACAC AACCGCCAGA CCCCCCCATC AGGACTCAĊA AACTACCACC GGTGCGCCAG CCACCTCGCA TTTGACCGCG ACCTGTCCAT GTCTTACTAC TCCTACGTTT GCTCTACGCC TCAACCTGGA GAGGAGAGGG CCAATCTCAT ACTITICTICA TTTGCCAAAT TTTGAAGAAC ATGATGTGGC TICCTICAGG TGGCCGAATC ACCAACGAGG AAGCTGCAGA GAAACTGATG **AACATGCTGA** GAGTGTGCAT GAATGCAATG AGAGCGGGCT GATGACTGGG ACCAGACTGT ATATCAAGAA ECOR1 ATCTCTCCCA CCCTTCTCCT TACTGGAATIT AAAAATGTG AATCAGTCAC TACATTTGGA CACCTTCTTC ACAGACCGCA ACCTCAACAC TATACTACTA CTGGCATCAC GTCCTAGCTG TTTCGGTCAC TATTCTGATT TACCAACACC CCCCATTCTA GAGGAAGAGA GACCCCGCCG TGTAACTTAC TCTCCCATAT TTCGGAATAA CCTACCAGGC ATATTCTTAT : CCTGAGTTT ACTCATGCAC CAGGCCACCT AACATTACTG CCTAACCGCT ATCGCTGTCG TACTCCGGAA ACTIATOATO TTCCCTCTAC ACCATTAACC AGCAATATCA GCGCCACCCT CTAATTGGAA CCAAGCCTAC TCGCCTTAAT GAAATCGCTG GACTATCCTA TAATTCTACT TTCACAATTC TTCTAGTAAG GTTTTCACAC

Fig. 8